

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/565,438  
Source: IFWP  
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IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/565,438

DATE: 08/11/2006  
TIME: 11:39:04

Input Set : A:\05101133.APP  
Output Set: N:\CRF4\08112006\J565438.raw

3 <110> APPLICANT: COSSON, BERTRAND  
4 PAILLARD, LUC  
5 LEGAGNEUX, VINCENT  
6 OSBORNE, HOWARD  
8 <120> TITLE OF INVENTION: PEPTIDE PROTEIN TRANSLATION INHIBITOR AND THE USE  
9 THEREOF FOR PROTEIN TRANSLATION CONTROL  
11 <130> FILE REFERENCE: 0510-1133  
13 <140> CURRENT APPLICATION NUMBER: 10/565,438  
14 <141> CURRENT FILING DATE: 2006-01-20  
16 <150> PRIOR APPLICATION NUMBER: PCT/FR04/050345  
17 <151> PRIOR FILING DATE: 2004-07-20  
19 <160> NUMBER OF SEQ ID NOS: 17  
21 <170> SOFTWARE: PatentIn Ver. 3.3  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 28  
25 <212> TYPE: PRT  
26 <213> ORGANISM: Xenopus laevis  
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32 Gln Gln Leu Gln Gln Gln Met Gln Gln Leu Asn Ala  
33 20 25  
36 <210> SEQ ID NO: 2  
37 <211> LENGTH: 28  
38 <212> TYPE: PRT  
39 <213> ORGANISM: Homo sapiens  
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45 Gln Gln Leu Gln Gln Gln Met Gln Gln Ile Ser Ala  
46 20 25  
49 <210> SEQ ID NO: 3  
50 <211> LENGTH: 84  
51 <212> TYPE: PRT  
52 <213> ORGANISM: Xenopus laevis  
54 <400> SEQUENCE: 3  
55 Phe Thr Thr Arg Ser Met Ala Gln Met Ala Ile Lys Ser Met His Gln  
56 1 5 10 15  
58 Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Ile Val Val Lys Phe Ala  
59 20 25 30  
61 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln  
62 35 40 45  
64 Gln Gln Met Gln Gln Leu Asn Ala Ala Ser Met Trp Gly Asn Leu Thr

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65 50 55 60  
 67 Gly Leu Asn Ser Leu Ala Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr  
 68 65 70 75 80  
 70 Ala Ser Ser Gly  
 74 <210> SEQ ID NO: 4  
 75 <211> LENGTH: 88  
 76 <212> TYPE: PRT  
 77 <213> ORGANISM: Homo sapiens  
 79 <400> SEQUENCE: 4  
 80 Phe Thr Thr Arg Ala Met Ala Gln Thr Ala Ile Lys Ala Met His Gln  
 81 1 5 10 15  
 83 Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Met Val Val Lys Phe Ala  
 84 20 25 30  
 86 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Ala Gln Gln Leu Gln  
 87 35 40 45  
 89 Gln Gln Met Gln Gln Ile Ser Ala Ala Ser Val Trp Gly Asn Leu Ala  
 90 50 55 60  
 92 Gly Leu Asn Thr Leu Gly Pro Gln Tyr Leu Ala Leu Tyr Leu Gln Leu  
 93 65 70 75 80  
 95 Leu Gln Gln Thr Ala Ser Ser Gly  
 96 85  
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 100 <211> LENGTH: 189  
 101 <212> TYPE: PRT  
 102 <213> ORGANISM: Artificial Sequence  
 104 <220> FEATURE:  
 105 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 106 fusion protein  
 108 <400> SEQUENCE: 5  
 109 Met Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Val Lys Phe Ala  
 110 1 5 10 15  
 112 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln  
 113 20 25 30  
 115 Gln Gln Met Gln Gln Leu Asn Ala Ala Ala Ala Met Ala Ser Asn Phe  
 116 35 40 45  
 118 Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr Gly Asp Val Thr Val  
 119 50 55 60  
 121 Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp Ile Ser Ser Asn  
 122 65 70 75 80  
 124 Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val Arg Gln Ser Ser  
 125 85 90 95  
 127 Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val Pro Lys Val Ala  
 128 100 105 110  
 130 Thr Gln Thr Val Gly Gly Glu Glu Leu Pro Val Ala Gly Trp Arg Ser  
 131 115 120 125  
 133 Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala Thr Asn Ser Asp  
 134 130 135 140  
 136 Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu Lys Asp Gly Asn  
 137 145 150 155 160

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139 Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile Tyr Gly Gly Gly  
140 165 170 175  
142 Gly Gly Ser Gly Pro Tyr Ser Ile Val Ser Pro Lys Cys  
143 180 185  
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147 <211> LENGTH: 154  
148 <212> TYPE: PRT  
149 <213> ORGANISM: Artificial Sequence  
151 <220> FEATURE:  
152 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
153 fusion protein  
155 <400> SEQUENCE: 6  
156 Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr  
157 1 5 10 15  
159 Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu  
160 20 25 30  
162 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser  
163 35 40 45  
165 Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu  
166 50 55 60  
168 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Glu Glu Leu Pro Val  
169 65 70 75 80  
171 Ala Gly Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
172 85 90 95  
174 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
175 100 105 110  
177 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
178 115 120 125  
180 Ile Tyr Gly Gly Gly Ser Lys Leu Gly Ser Met Ala Tyr Pro  
181 130 135 140  
183 Tyr Asp Val Pro Asp Tyr Ala Arg Ala Ala  
184 145 150  
187 <210> SEQ ID NO: 7  
188 <211> LENGTH: 570  
189 <212> TYPE: DNA  
190 <213> ORGANISM: Artificial Sequence  
192 <220> FEATURE:  
193 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
194 fusion polynucleotide  
196 <400> SEQUENCE: 7  
197 atggcttacc catacagatgt tccagattac gctagcgtaa agttcgacaga cactcagaaa 60  
198 gacaaagaac agaagcgcat gacgcagcaa cttcagcagc aaatgcagca gctcaatgca 120  
199 gccccgcaca tggcttctaa cttaactcag ttcgttctcg tcgacaatgg cgaaactggc 180  
200 gacgtgactg tcgccccaaag caacttcgct aacggggtcg ctgaatggat cagctctaac 240  
201 tcgcgatcac aggttacaa agtaaacctgt agcgttcgtc agagctctgc gcagaatcgc 300  
202 aaatacaccca tcaaagtctga ggtgcctaaa gtggcaaccc agactgttgg tggtaagag 360  
203 cttcctgttag ccggatggag atcttactta aatatggaac taaccattcc aattttcgcc 420  
204 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480  
205 ccgattccct cggccatcgc ggcacactcc ggcacatcagc gaggtggagg tggatctggg 540

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206 ccctattcta tagtgtcacc taaatgctag 570  
 209 <210> SEQ ID NO: 8  
 210 <211> LENGTH: 570  
 211 <212> TYPE: DNA  
 212 <213> ORGANISM: Artificial Sequence  
 214 <220> FEATURE:  
 215 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 216 fusion polynucleotide  
 218 <400> SEQUENCE: 8  
 219 atggcttacc catacgatgt tccagattac gctagcgtaa aatttgctga tacacagaag 60  
 220 gacaaagaac agaagagaat ggcccagcag ctccagcgc agatgcgc aatcagcgca 120  
 221 gccggccgcctaa tggcttctaa ctttactcgat ttcgttctcg tcgacaatgg cggaactggc 180  
 222 gacgtgactg tcgccccaaag caacttcgt aacggggtcg ctgaatggat cagctctaacc 240  
 223 tcgcgatcac aggcttacaa agtaacctgt agcgttcgtc agagctctgc gcagaatcgc 300  
 224 aaatacaccca tcaaagtctga ggtgcctaaa gtggcaaccc agactgttgg tggtaagag 360  
 225 cttcctgttag ccggatggag atcttactta aatatggAAC taaccattcc aatttcgccc 420  
 226 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480  
 227 ccgattccct ccggccatcgc ggccaaactcc ggcatctacg gaggtggagg tggatctggg 540  
 228 ccctattcta tagtgtcacc taaatgctag 570  
 231 <210> SEQ ID NO: 9  
 232 <211> LENGTH: 489  
 233 <212> TYPE: PRT  
 234 <213> ORGANISM: Xenopus laevis  
 236 <400> SEQUENCE: 9  
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 238 1 5 10 15  
 240 Lys Met Phe Val Gly Gln Val Pro Arg Ser Trp Ser Glu Lys Glu Leu  
 241 20 25 30  
 243 Arg Glu Leu Phe Glu Gln Tyr Gly Ala Val Tyr Glu Ile Asn Val Leu  
 244 35 40 45  
 246 Arg Asp Arg Ser Gln Asn Pro Pro Gln Ser Lys Gly Cys Cys Phe Ile  
 247 50 55 60  
 249 Thr Phe Tyr Thr Arg Lys Ala Ala Leu Glu Ala Gln Asn Ala Leu His  
 250 65 70 75 80  
 252 Asn Met Lys Val Leu Pro Gly Met His His Pro Ile Gln Met Lys Pro  
 253 85 90 95  
 255 Ala Asp Ser Glu Lys Asn Asn Ala Val Glu Asp Arg Lys Leu Phe Ile  
 256 100 105 110  
 258 Gly Met Val Ser Lys Asn Cys Asn Glu Asn Asp Ile Arg Ala Met Phe  
 259 115 120 125  
 261 Ser Pro Phe Gly Gln Ile Glu Glu Cys Arg Ile Leu Arg Gly Pro Asp  
 262 130 135 140  
 264 Gly Met Ser Arg Gly Cys Ala Phe Val Thr Phe Thr Thr Arg Ser Met  
 265 145 150 155 160  
 267 Ala Gln Met Ala Ile Lys Ser Met His Gln Ala Gln Thr Met Glu Gly  
 268 165 170 175  
 270 Cys Ser Ser Pro Ile Val Val Lys Phe Ala Asp Thr Gln Lys Asp Lys  
 271 180 185 190  
 273 Glu Gln Lys Arg Met Thr Gln Gln Leu Gln Gln Met Gln Gln Leu

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274 195 200 205  
 276 Asn Ala Ala Ser Met Trp Gly Asn Leu Thr Gly Leu Asn Ser Leu Ala  
 277 210 215 220  
 279 Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr Ala Ser Ser Gly Asn Leu  
 280 225 230 235 240  
 282 Asn Ser Leu Ser Gly Leu His Pro Met Gly Ala Glu Tyr Gly Thr Gly  
 283 245 250 255  
 285 Met Thr Ser Gly Leu Asn Ala Ile Gln Leu Gln Asn Leu Ala Ala Leu  
 286 260 265 270  
 288 Ala Ala Ala Ala Ser Ala Ala Gln Asn Thr Pro Ser Ala Gly Ala Ala  
 289 275 280 285  
 291 Leu Thr Ser Ser Ser Pro Leu Ser Ile Leu Thr Ser Ser Gly Ser  
 292 290 295 300  
 294 Ser Pro Ser Ser Asn Asn Ser Ser Ile Asn Thr Met Ala Ser Leu Gly  
 295 305 310 315 320  
 297 Ala Leu Gln Thr Leu Ala Gly Ala Thr Ala Gly Leu Asn Val Asn Ser  
 298 325 330 335  
 300 Leu Ala Gly Met Ala Ala Phe Asn Gly Gly Leu Gly Ser Ser Leu Ser  
 301 340 345 350  
 303 Asn Gly Thr Gly Ser Thr Met Glu Ala Leu Ser Gln Ala Tyr Ser Gly  
 304 355 360 365  
 306 Ile Gln Gln Tyr Ala Ala Ala Leu Pro Ser Leu Tyr Asn Gln Ser  
 307 370 375 380  
 309 Leu Leu Ser Gln Gln Gly Leu Gly Ala Ala Gly Ser Gln Lys Glu Gly  
 310 385 390 395 400  
 312 Pro Glu Gly Ala Asn Leu Phe Ile Tyr His Leu Pro Gln Glu Phe Gly  
 313 405 410 415  
 315 Asp Gln Asp Leu Leu Gln Met Phe Met Pro Phe Gly Asn Val Val Ser  
 316 420 425 430  
 318 Ser Lys Val Phe Ile Asp Lys Gln Thr Asn Leu Ser Lys Cys Phe Gly  
 319 435 440 445  
 321 Phe Val Ser Tyr Asp Asn Pro Val Ser Ala Gln Ala Ala Ile Gln Ser  
 322 450 455 460  
 324 Met Asn Gly Phe Gln Ile Gly Met Lys Arg Leu Lys Val Gln Leu Lys  
 325 465 470 475 480  
 327 Arg Ser Lys Asn Asp Ser Lys Pro Tyr  
 328 485  
 331 <210> SEQ ID NO: 10  
 332 <211> LENGTH: 1470  
 333 <212> TYPE: DNA  
 334 <213> ORGANISM: Xenopus laevis  
 336 <400> SEQUENCE: 10  
 337 atgaatggca caatggacca cccagaccat ccggatccgg actccatcaa gatgtttgtg 60  
 338 ggtcagggttc ctcgaagctg gtcagagaaa gagctaagag aactcttcga gcagtacgga 120  
 339 gccgtctatg aaattaatgt tctccgagac agaagccaga atcctcctca gagcaaagga 180  
 340 tgctgtttta ttactttcta cacaagaaaa gctgcgttag aagcacagaa tgctttgcac 240  
 341 aacatgaaag ttctccctgg gatgcatcat ccaatacaga tgaagccagc cgacagtgaa 300  
 342 aagaataatg ctgtgaaaga ccgaaagcta tttatcgaa tggtttccaa gaattgtaat 360  
 343 gagaatgata tccggccat gttctctccg tttggacaga tagaggaatg tcgtatcctg 420

**VERIFICATION SUMMARY**

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